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FIG. 1A

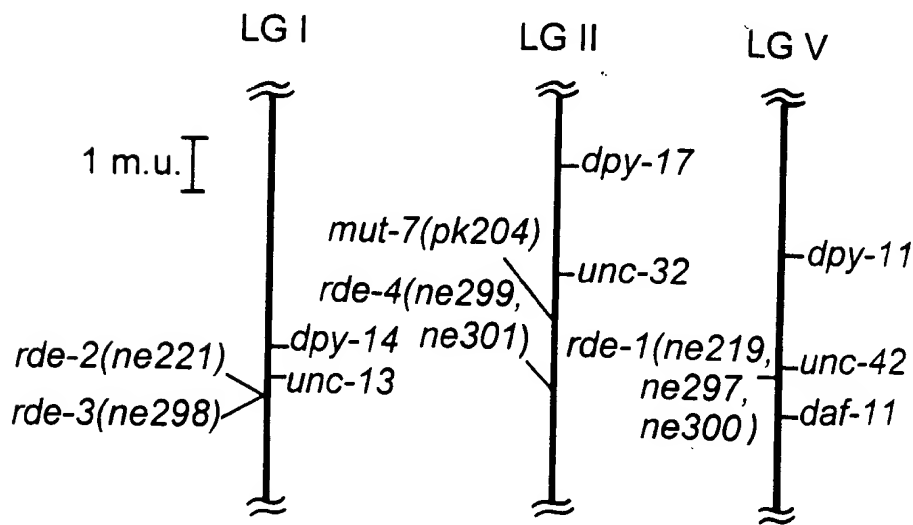


FIG. 1B

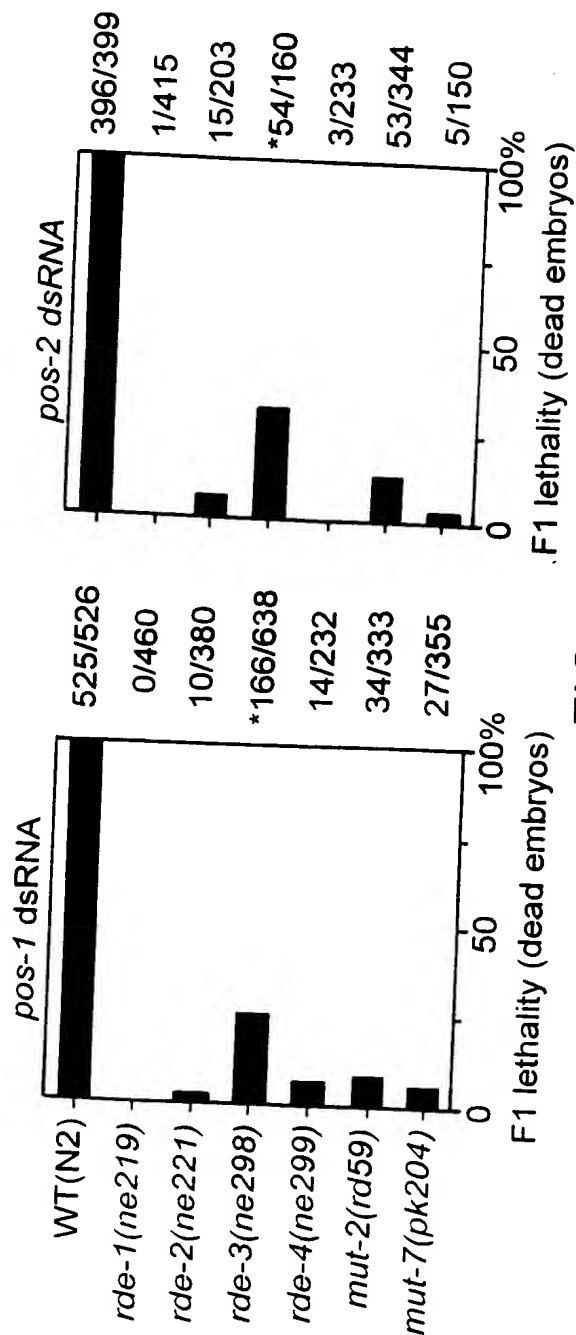
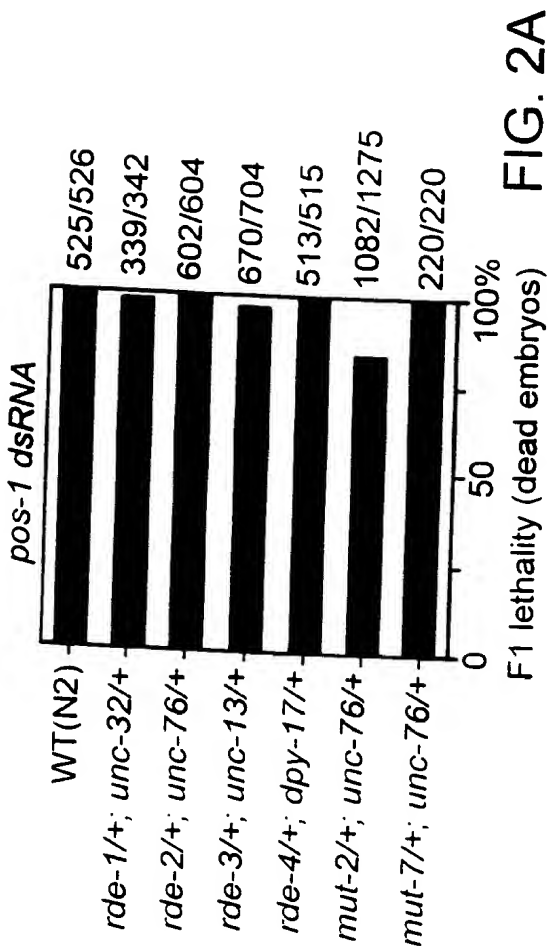


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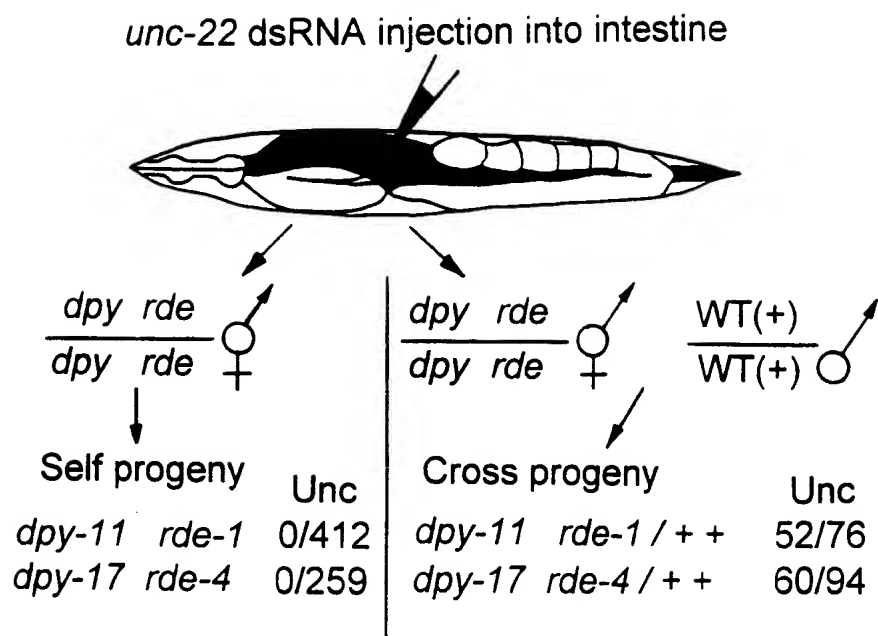


FIG. 3



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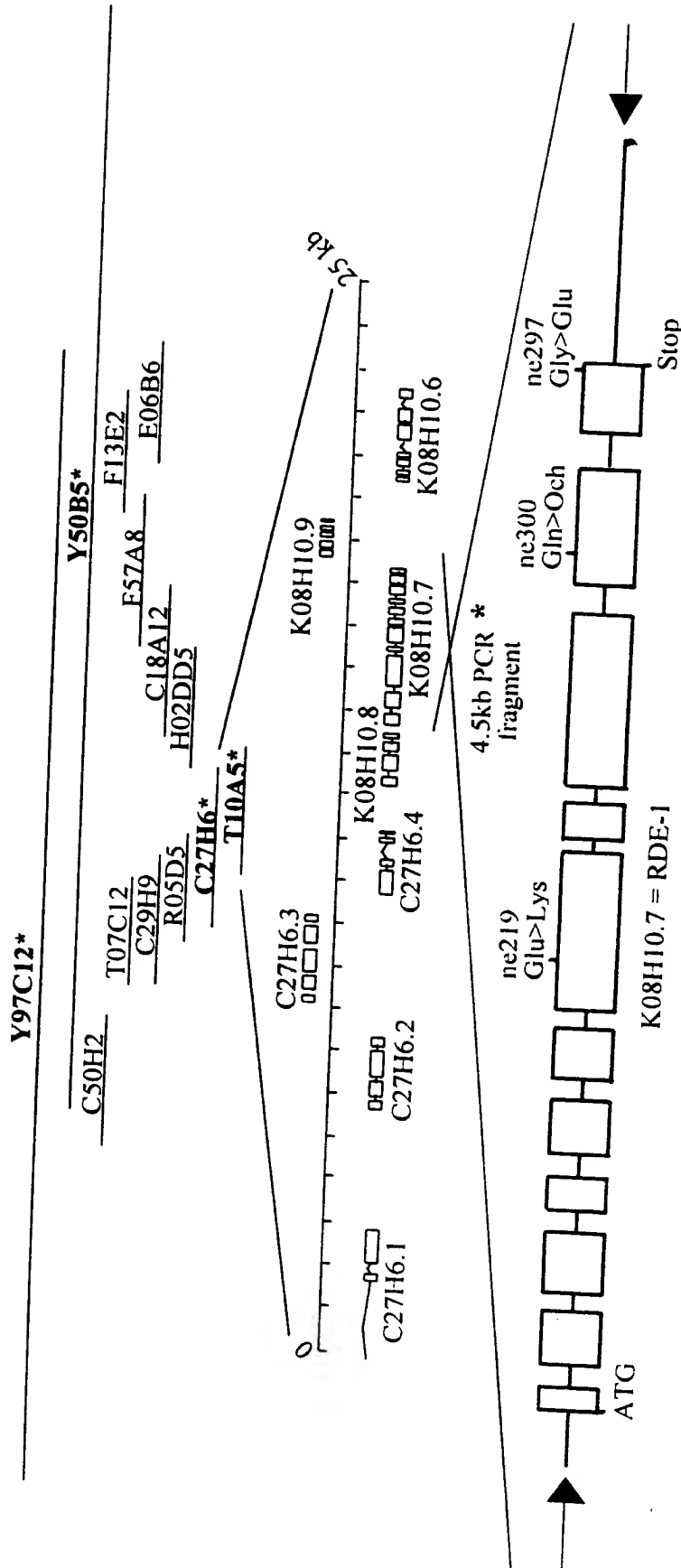


FIG. 4A



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RDE-1 514 QLNVPKEKELCCAVFVNE TAGNPCLEENDVWKEYTELIGGCKFRGIRIGANENRGAQSIMYDATKNEAFYKKNCTLNTGIGRFEIAATE
F48F7.1 581 RGKQFHTGIDVRVWAIACFAQ-CQHYKENDLRMEFNCLORI SNDAGPIVGNPCFCKYAVGVEQVAPMFKYIAQNTSG
eIF2C 392 RNKQFHTGIEIKWALACFA-P-DRQCTEVHLKSETELRKSRDAGP-IOQPCFCKYAGGADSVGPMFRHLKNTYAG
ZWILLE 542 MNKRMINGMTVSRVACVNF8---RSVQENVARGFCELGQCEVSGEENPEFVPIYISARPDQVEKALKHVIYHTSMNKT
Sting 482 RTCSMFKNVHINRWYVITPS---RNLR--ETQEFVQCI RTASSMKMNICNPIYEEIPDDRNGTYSQAIDNAAAN---
RDE-1 604 AKNMFERLPDKEQKVFMEFIISKRLQNAAGFVRHYCDHTIGVANOHISSETVTRALASLRHEKSGKRIFYQIAKINAKLGGINQEDWS
F48F7.1 658 ---IQLVVWVLRG-KTPVMAEVRVGDVILGTAGQCVGAIAIRTP
eIF2C 469 ---LQTVVWVLRG-KTPVMAEVRVGDVILGTAGQCVGAIAIRTP
ZWILLE 620 ---GKELELLALLPDNNGSLYGDILKRIQETELGLISOCCLTKHVFISK
Sting 552 ---DPQIVMVVRSPNEEKYSCKIKRTICVDRPVPSSOVVTLKVIAPRQ---KPTGLMSIATKVVIQMNKLMGAP
RDE-1 694 EIAEISPEEKERRKTMPLTMYVGIDVTHPTSYSQIDYSIAAASINPGGT-ITRNMIVTQEECRPGERAVAHGRE---RTDILEAKFVK
F48F7.1 725 V---RPRIFNEPVIFFGCDITHPAGDSRRKPSIAAAGSADAPPS-RYAAATRVQCHROEII SDITY---MYRE
eIF2C 536 G---RPPVTOQPVIFIGADVTHPPAGDCKKPSIAAASADAPPN-RYCAATRVQCHROEIIQDIAA---MYRE
ZWILLE 691 IS---CRIPLYSDIPITITFGADVTHPENGEESSPSIAAASADAPPEVTKVAGLVCAQAHROELIODLYKTWQDPVPGTVSGGMIRD
Sting 621 W---QVVIPLHGLMTVGFDVCHSP--KNKNKSYCAFYATMDQKESFRIFSTVNEHIKGOEISEQMSVN---MAC

FIG. 4B-2



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* ne300

| | | | | | | | | |
|---------|-----|------------------|---------------------|------------------|------------------|----------------|--------------|-------------|
| RDE-1 | 780 | LLREFAENNDNRAPAH | IIIVYRDGVSDSEMLRVSH | DELRSIKSEVKQFMSE | RGEDPEPKYTF | IVIOKRHNTR | LLRRMEKDKPVV | NKDLTP |
| F48F7.1 | 792 | LLVQFYRNTR | FKPARIVVYRDGVSE | GFNNVLOVELRA | IREACMLERGYQPG | --- | ITFIIVOKRRH | TRRLAVDKKDO |
| eIF2C | 603 | LLICQFYKSTR | FKPTRLIIFYRDGVSE | GFNNVLOVELRA | IREACMLERGYQPG | --- | ITFIIVOKRRH | TRRLAVDKKDO |
| ZWILLE | 775 | LLISERKATG | QKPLRIIFRYRDGVSE | GFNNVLOVELRA | IREACMLERGYQPG | --- | ITFIIVOKRRH | TRRLAVDKKDO |
| Sting | 687 | ALLRSYQEQHR | SLPERIIFFRDGVGD | GLIYQVNSEVNTI | KDLDEIYKSAGKQEGC | RMTEIISKRINSRY | ETGHRNPV | --- |
| RDE-1 | 870 | AETDVAVAAVKQWEED | MKESKETGIVNPSS | GTIVDVKILIVSKYK | FEFFLASHHGVLG | TSRPGHYIVMYDD | KGMSODEVYK | TYGIAFLSAR |
| F48F7.1 | 868 | --- | --- | --- | --- | --- | --- | --- |
| eIF2C | 679 | --- | --- | --- | --- | --- | --- | --- |
| ZWILLE | 853 | --- | --- | --- | --- | --- | --- | --- |
| Sting | 766 | --- | --- | --- | --- | --- | --- | --- |
| RDE-1 | 960 | CRKPTSLPVEVHYAHL | SCEKALVYR | TYKEHYICDYAQP | TRHEMEHFLQTNV | KYPGMSFA | --- | --- |
| F48F7.1 | 936 | CTRSVSIIPAPAYYAH | LVAFRAHYHLVDRE | HDSCGSGQSGT | SEDTLSNMARAVQ | VILAE | NLVSI | --- |
| eIF2C | 747 | CTRSVSIIPAPAYYAH | LVAFRAHYHLVDRE | HDSCGSGQSGT | SEDTLSNMARAVQ | VILAE | NLVSI | --- |
| ZWILLE | 921 | CTRSVSIIPAPAYYAH | LVAFRAHYHLVDRE | HDSCGSGQSGT | SEDTLSNMARAVQ | VILAE | NLVSI | --- |
| Sting | 827 | YSGTIRVPAVCHYAH | KLAPLVAES | INRAPSAGLQ | NQLYFL | --- | --- | --- |

FIG. 4B-3



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cagccacaaagtgatgaacaatgtccctcgaaatttcccgaaattggaaaaaggattttatcgctcattctctcgatccggta
tgcataattattagcagctataagatatataagtttgatattataattatattatagggagatgaaatggcttgcgagggccccactg
gtaaatgcgcggcacaattctatgagaagaaagtagtactctcttttggtaaatgtgttcaagtctctccagcaaaaattttacgat
cgggaatactactacgagtatgaaagtgaataatgacaaaaggaaagtattgaatagaaaaaccaggaaaaacctttcccaaaaaag
agaaattccaatgtaatgtgtgttaaatgtatgtaaaaactaatttatttttcagtcgccgacgtgcgaaaaactctctctggc
aacatcttcggcatgagaagacagacagattttattctcgaaagactatgtttttgatgaaaaaggcacactgtttatagt
gtttgtcgactgaacactgtcacatcaaaaaatgtcgtgttcgggagaaagtagtaaaaaaggattcgggagaaaaaagatg
aaaggatttggagaaaaaaatcttatacacaatgatacttacctatcgtaaaaaatttcacctgaactttagtcgagaaa
atccggaaaaagacggaagcgaatcggaggttacaaattccctgaagggtttatgaaaaacacgcattatacaaaaacaa
ttagctttcagaatgttatgacccagaaagtctgctacgcgccttttgtaacgaggagattaaagtgtgagttgcaata
ataataataataatcacctcaactcatttatattttaagacaattcgcgaaaaaattttgtgtacgataataattcaat

FIG. 5A



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tctgcgagttcctgaatcgtttcacgatccaaacagattcgaacaatcattagaagtagcaccaagaatcgaagcatggt
ttggaatttacattggaaatcaaagaattgttcgatggggaacctgtgtcatttttgcaagtaagtttgagaaactgcga
taaaaaatcatgtgattttgtgaagttgtcgataaactattctacaatgcaccgaaaatgtctcttctggattatctt
ctcctaattgtcgacccccagtcgtgtaacgatgatgtacgaaaagatcttaaaacaaaactgtatggcgaggaaaaatgac
aatcagacaagccgcgcggccaagaattcgacaattattggaaaatttgaagctgaaatgcgcagaagtttgggataac
aaatgttagtttaaatattcacaataatatacaaatgtatttcaggctcgagattgacagaacgacatctgacatt
tctagatttgtgcgaggaaaactctctgtttataaagtcactggtaaatcggacagaggaagaaatgcaaaaaagtacg
atactacattgttcaaaaatctatgaggaaaacaaaaagttcattgagtttccccacctaccactagtcaaaagttaaaagt
ggagcaaaaagaatacgtgtaccaatggaacatcttgaagttcatgagaagccacaaagatacaagaatcgaattgatc
ggatgatcaagacaagtttctaaagcgagctacacgaaaacctcagactacaaagaaaataccctaaaaatgttgaaa
aattggatttctcttctgaagagctaaattttgtgaaagatttggattatgtccaaacttcagatgatcgaatgtcca
ggaaagggttttgaagagccaatgcttgtgaatagtgtaaatgaacaaattaaatgacaccagtgattcgtggatttca
agaaaaacaattgaatgtggttcccgaaaaagaacttctgtgtgtgtttttagtcaacgaaacagcgggaaatccat
gcttagaagagaacgacgttgtgtaagtgtttctacgtagattattccgaaatatttcagtaagttctacaccgaact
aattggtggttgaagttccgtggaatacgaattggtgccaatgaaaacagaggagcgaatctattatgtacgacgcga
cgaaaaatgaatatgccgtaagtttcagaaaattgaaagtttttaaatatcatatttacagttctacaaaaattgtacac
taaataccggaatcggtagatttgaaatagccgcaacagaagcgaagaatatgtttgaacgtcttcccgataaagaaca
aaagcttaatgttcattatcatttccaaacgacaactgaatgcttacgggtttgtgaaacattattgcgatcacacat
cgggttagctaatcagcatattacttctgaaacagtcacaaaagctttggcatcactaaggcacgagaaaggatcaaaac
gaattttctatcaaattgcattgaaaatcaacgcgaaattaggagggtattaccaggagcttgactggtcagaaattgca
gaaatatcaccagaagaaaaagaaagacggaaaacaatgccattaactatgtatgttgaattgatgtaactcatcaa
ctctacagtggaaattgattattctatagcggctgtagtagcgagratcaatccagggtggaactatctatcgaaatatga
ttgtgactcaagaagaargtcgtcccggtgagcgtgcagtggtcatggacgggaaagaacagatatttggaaagcaaa
ttcgtgaaattgtcagagaattcgcagaagtgagttgtcttgagrattttaaaagatctctgggaattttaattttttg

FIG. 5B

(SEQ ID NO:1)

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Appln No.: 09/689,992

Applicant(s): Craig C. Mello et al.

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RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR
TARGETED GENETIC INTERFERENCE

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CAGCCACAAAGTGATGAAC- 5' UTR

1/1

ATG TCG TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn pro pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21

ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41

CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CCG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61

TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81

AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101

AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121

AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141

AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161

CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181

GAA GCG AAT CCG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CCG TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201

CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221

TCA ATT CTG CGA GTT COT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241

781/281

FIG. 6A

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731/261
GTA GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT
val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp

811/271
GGT GAA COT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG
gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met

841/281
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA
ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg

901/301
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA
lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro

961/321
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA
arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu

1021/341
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT
met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu

1081/361
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA
val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys tyr asp thr thr

1141/381
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC
leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val

1201/401
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG
lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu

1261/421
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA
lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg

1321/441
GCT ACA CGA AAA COT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT
ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp

1381/461
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG
phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met

1441/481
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA
ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln

1501/501
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA
ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

FIG. 6B

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1561/521
AAA GAA GTT TGC TGT GGT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT GCA TGC TTA GAA
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1621/541
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

1681/561
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT
arg ile gly ala asn glu asn arg gly ala gin ser ile met tyr asp ala thr lys asn

1741/581
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

1901/601
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gin lys val leu met

1861/621
TTC ATT ATC ATT TCC AAA GCA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT
phe ile ile ile ser lys arg gin leu asn ala tyr gly phe val lys his tyr cys asp

1921/641
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA
his thr ile gly val ala asn gin his ile thr ser glu thr val thr lys ala leu ala

1981/661
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC
ser leu arg his glu lys gly ser lys arg ile phe tyr gin ile ala leu lys ile asn

2041/681
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA
ala lys leu gly gly ile asn gin glu leu asp trp ser glu ile ala glu ile ser pro

2101/701
GAA GAA AAA GAA AGA GCG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

2161/721
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

2221/741
CCA GGT GGA ACT ATC TAT GCA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT CAG
pro gly gly thr ile tyr arg asn met ile val thr gin glu glu cys arg pro gly glu

2281/761
CGT GCA GTG GCT CAT GGA CCG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

2341/781
CTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

FIG. 6C

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2401/801
SAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA
asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2431/811
2461/821
AGC GAA GTA AAA CAA TTC ATG TCG GAA CCG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG
ser glu val lys gln phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr

2491/831
2521/841
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG
phe ile val ile gln lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2551/851
2581/861
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA
pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala val lys

2611/871
2641/881
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA
gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2671/891
2701/901
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT
thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2731/911
2761/921
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA
his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2791/931
2821/941
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT
met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2851/951
2881/961
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG
arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2911/971
2941/981
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CCG ACT
lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

2971/991
3001/1001
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA
arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3031/1011
3061/1021
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT
OCH (SEQ ID NO:3)

3091/1031
3121/1041
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3151/1051
3181/1061
CTT GAA ATT TAA AAA AAA AAA AAA (SEQ ID NO:2)

FIG. 6D

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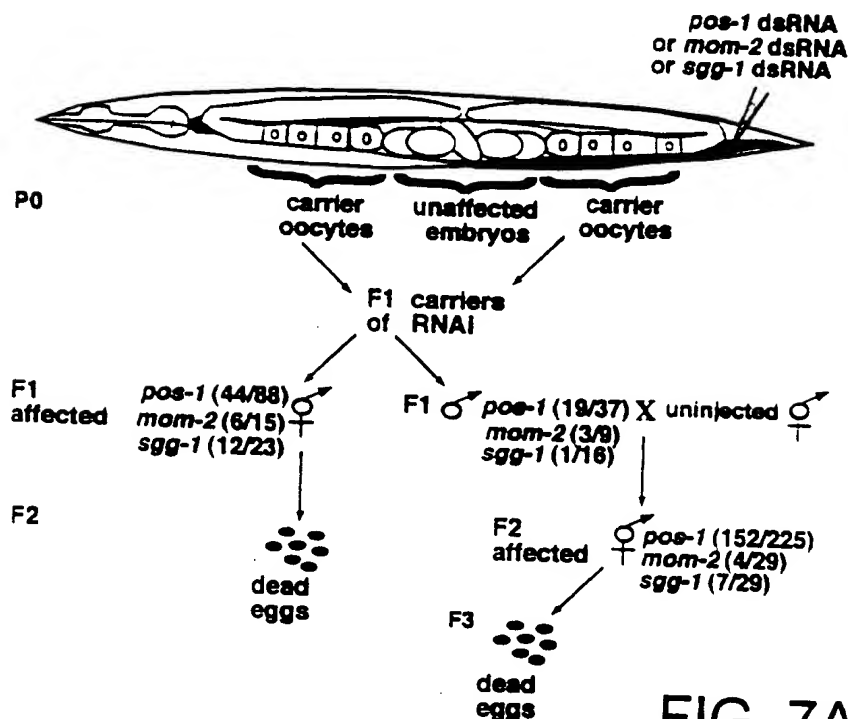


FIG. 7A

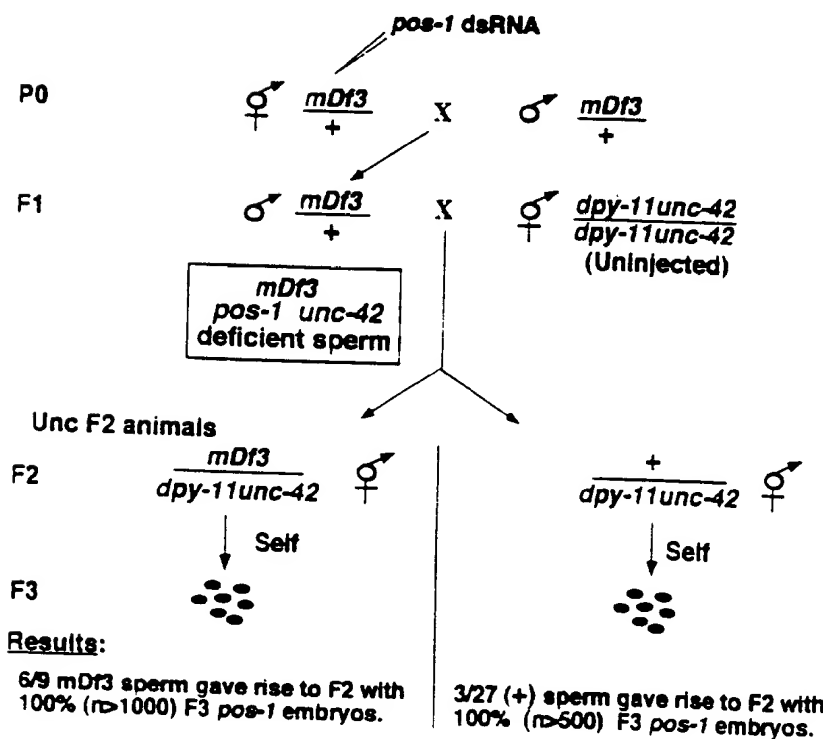


FIG. 7B



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| Injected P0 | | F1 | |
|------------------------------------|--------|-------------|-------|
| ♀ $\frac{rde-1 \text{ unc-42}}{+}$ | self X | $rde-1 (-)$ | 11/24 |
| | | $rde-1 (+)$ | 9/72 |
| ♀ $\frac{rde-2 \text{ unc-13}}{+}$ | | $rde-2 (-)$ | 0/39 |
| | | $rde-2 (+)$ | 23/78 |
| ♀ $\frac{mut-7 \text{ dpy-17}}{+}$ | | $mut-7 (-)$ | 0/15 |
| | | $mut-7 (+)$ | 20/50 |
| ♀ $\frac{rde-4 \text{ unc-69}}{+}$ | | $rde-4 (-)$ | 5/15 |
| | | $rde-4 (+)$ | 11/48 |

FIG. 8A

| P0 | Injected F1 |
|------------------------------------|--|
| ♀ $\frac{rde-1 \text{ unc-42}}{+}$ | $\frac{rde-1 \text{ unc-42}}{rde-1 \text{ unc-42}}$ 0/37 |
| ♀ $\frac{rde-4 \text{ unc-69}}{+}$ | $\frac{rde-4 \text{ unc-69}}{rde-4 \text{ unc-69}}$ 0/37 |

FIG. 8B



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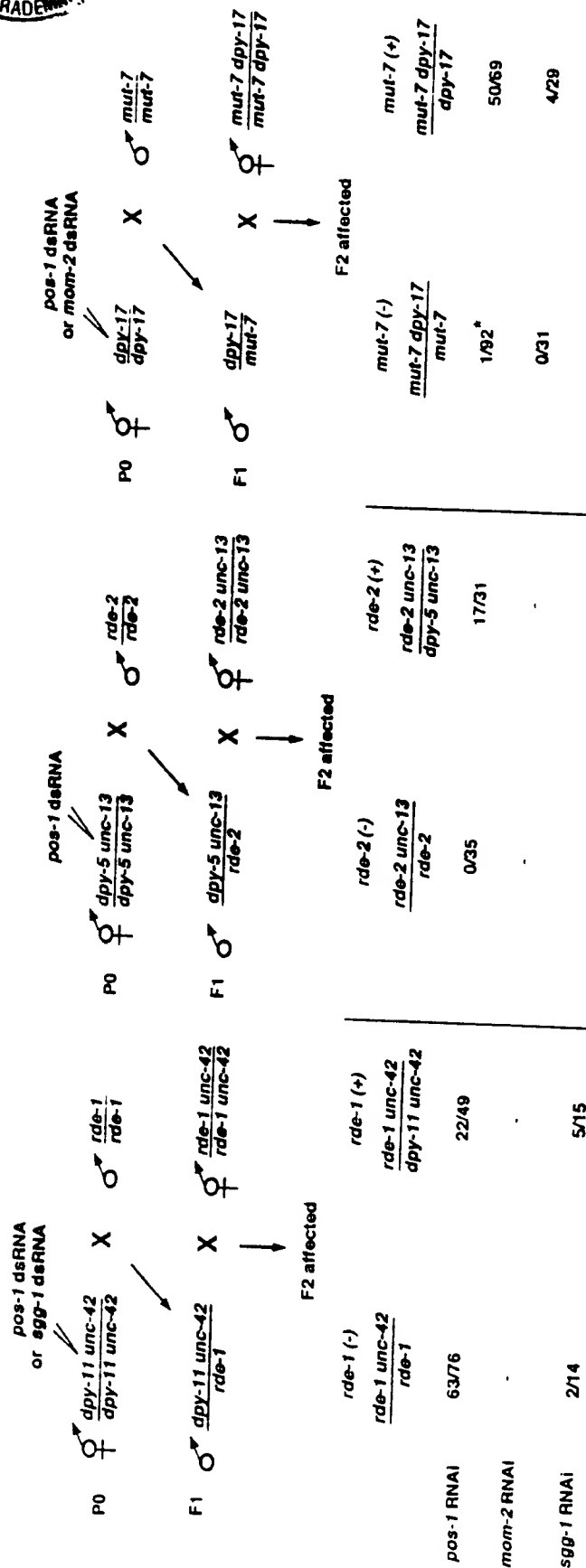


FIG. 9A

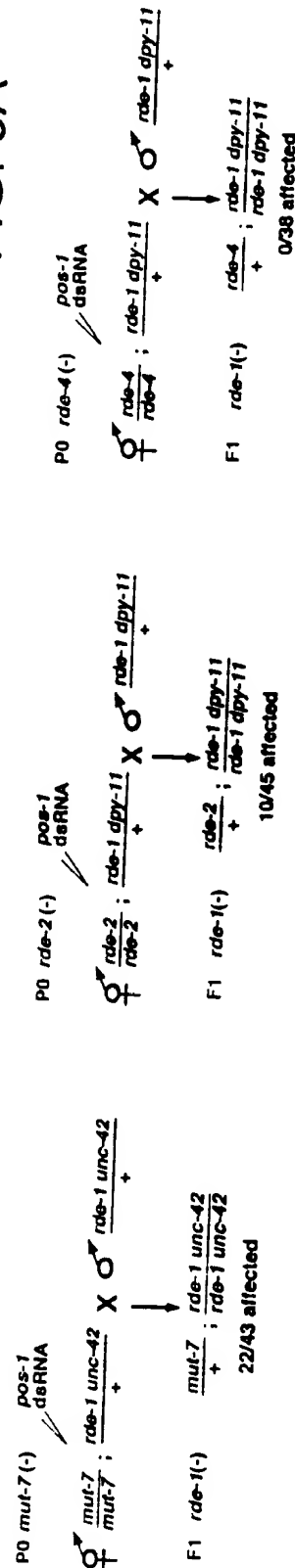


FIG. 9B

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10 20 30 40 50 60
ATGGATTTAACCAACTAACGTTTGAAGCGTTTTCGGTGGATCAGATGTTCCCTATGAAG
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTTGGAGATGTTTCTG
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180
AAGAAACTCCCCTCATGGTACTAGAGAGGCTGCTAAGGCTGTCTATCAAAGACGCCA
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240
ACTTGGGGCACTGTGCAACTTCCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTTCATTCTGGAACAACCAAA
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420
GAAGAAGCTCTTTTGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480
ACTTCAGATGCTGTTTCAGGATAACGATAACGATGATTGCTTCTACAAAGTCTGAATTT
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540
CCACCTGGTATTTTCGCCAACCAGAGAATTGGGTTCGGAAAGTTGCAGGAAAAATCTCAAAAA
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAATGAGAGAACCGAGCGTTTCTTG
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660
GTTATATGACGATGTGCAATCAAAAAACCGAGGAATCAGAAGTAAGAAGAAGGACGCA
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720
AAGAATCTTGCAGCATGGTTGATGTGGAAGCGTTGGAAGACGGTATCGAATCTCTGGAA
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT
S Y D M V D V I E N L E E A E H L L E I

FIG. 10A



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790 800 810 820 830 840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCGGCACTGATTGATATACTCTCGGAC
Q D Q A S K I K D K H S A L I D I L S D

850 860 870 880 890 900
AAGAAAAGATTTTCAGACTACAGCATGGATTTCAACGTATTATCAGTGAGCACAATGGGA
K K R F S D Y S M D F N L S V S T M G

910 920 930 940 950 960
ATACATCAGGTGCTATTGGAAATCTCGTTCCGGCGTCTAGTTTCTCCAGACCCCGACGAT
I H Q V L L E I S F R R L V S P D P D D

970 980 990 1000 1010 1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L E M G A E H T Q T E E I M K A T A E K

1030 1040 1050 1060 1070 1080
GAAAAGCTACGGAAGAAGAATATGCCAGATTCCGGGCCGCTAGTGTGCTGGACATGGT
E K L R K K N M P D S G P L V F A G H G

1090 1100 1110 1120 1130 1140
TCATCGGGCGGAAGAGGCTAAACAGTGTGCTTGTAATCGGCGATTATCCATTTCAACACC
S S A E E A K Q C A C K S A I I H F N T

1150 1160 1170 1180 1190 1200
TATGATTTTACGGATTGAAAATATTATTGCGTATTCCTGAAAAATGAAGCGTCTGAATGA
Y D F T D * K Y Y C V F L K N E A S E *

1210 1220 1230
TTATAAAAAAAAAAAAAAAAAA
L * K K K K K

(SEQ ID NO:4)
(SEQ ID NO:5)

FIG. 10B

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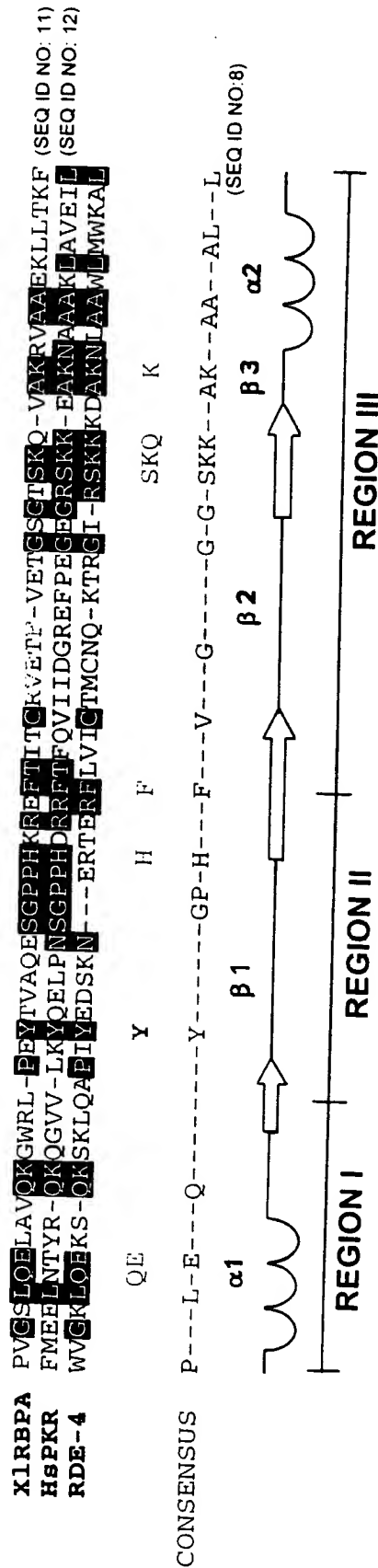


FIG. 11



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FIG. 12 Rescue of *rde-4*:

